



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Atty. Docket No: 065691/0222

Patent application of

CHAMBON, PIERRE et al.

Serial No. 09/853,033

Filed: May 11, 2001

For: TRANSGENIC MOUSE FOR TARGETED RECOMBINATION MEDIATED
BY MODIFIED CRE-ER

STATEMENT TO SUPPORT FILING AND SUBMISSION IN
ACCORDANCE WITH 37 C.F.R. §§ 1.821-1.825

Assistant Commissioner for Patents
Washington, D.C. 20231
Box SEQUENCE

Sir:

In connection with a Sequence Listing submitted concurrently herewith, the undersigned hereby states that:

1. the submission, filed herewith in accordance with 37 C.F.R. § 1.821(g), does not include new matter;
2. the content of the attached paper copy and the attached computer readable copy of the Sequence Listing, submitted in accordance with 37 C.F.R. § 1.821(c) and (e), respectively, are the same; and
3. all statements made herein of their own knowledge are true and that all statements made on information and belief are believed to be true; and further, that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United

Serial No. 09/853,033

States Code and that such willful false statements may jeopardize the validity of the application or any patent resulting therefrom.

Respectfully submitted,


Date 26, 2001


James A. Coburn

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Intellectual Property Services
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Portsmouth, N.H.
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Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr Ser	
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Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu Ser	
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His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser Met	
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Lys Cys Lys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Met Leu	
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 Homosapiens-Bacteriophage P1

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gat cgc cag gcg ttt tct gag cat acc tgg aaa atg ctt ctg tcc gtt 144
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 Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
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 Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala
 65 70 75 80

cgc ggt ctg gca gta aaa act atc cag caa cat ttg ggc cag cta aac 288
 Arg Gly Leu Ala Val Lys Thr Ile Gln His Leu Gly Gln Leu Asn
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10883033.000001

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ggt	cgt	tca	ctc	atg	gaa	aat	agc	gat	cgc	tgc	cag	gat	ata	cgt	aat	480
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Ile	Ala	Arg	Ile	Arg	Val	Lys	Asp	Ile	Ser	Arg	Thr	Asp	Gly	Gly	Arg	
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310																
315																
320																

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 Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu
 565 570 575

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 580 585 590

atg aag tgc aag aac gtg gtg ccc ctc tat gac ctg ctg ctg gag atg 1824
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 595 600 605

ctg gac gcc cac cgc cta cat gcg ccc act agc cgt gga ggg gca tcc 1872
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 610 615 620

gtg gag gag acg gac caa agc cac ttg gcc act gcg ggc tct act tca 1920
 Val Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser
 625 630 635 640

tcg cat tcc ttg caa aag tat tac atc acg ggg gag gca gag ggt ttc 1968
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 <223> Description of Artificial Sequence: Chimeric sequence
 Homosapiens-Bacteriophage P1

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 35 40 45
 Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
 50 55 60
 Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala
 65 70 75 80

00653033.0008001

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Val	Ser	Leu	Val	Met	Arg	Arg	Ile	Arg	Lys	Glu	Asn	Val	Asp	Ala	Gly	
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Tyr	Gly	Ala	Lys	Asp	Asp	Ser	Gly	Gln	Arg	Tyr	Leu	Ala	Trp	Ser	Gly	
				275					280					285		
His	Ser	Ala	Arg	Val	Gly	Ala	Ala	Arg	Asp	Met	Ala	Arg	Ala	Gly	Val	
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Ser	Ile	Pro	Glu	Ile	Met	Gln	Ala	Gly	Gly	Trp	Thr	Asn	Val	Asn	Ile	
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<212> DNA

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Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg
180 185 190

atg tta atc cat att ggc aga acg aaa acg ctg gtt agc acc gca ggt Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly 195 200 205	624
gta gag aag gca ctt agc ctg ggg gta act aaa ctg gtc gag cga tgg Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp 210 215 220	672
att tcc gtc tct ggt gta gct gat gat ccg aat aac tac ctg ttt tgc Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys 225 230 235 240	720
cgg gtc aga aaa aat ggt gtt gcc gcg cca tct gcc acc agc cag cta Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu 245 250 255	768
tca act cgc gcc ctg gaa ggg att ttt gaa gca act cat cga ttg att Ser Thr Arg Ala Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Ile 260 265 270	816
tac ggc gct aag gat gac tct ggt cag aga tac ctg gcc tgg tct gga Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly 275 280 285	864
cac agt gcc cgt gtc gga gcc gcg cga gat atg gcc cgc gct gga gtt His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val 290 295 300	912
tca ata ccg gag atc atg caa gct ggt ggc tgg acc aat gta aat att Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile 305 310 315 320	960
gtc atg aac tat atc cgt aac ctg gat agt gaa aca ggg gca atg gtg Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val 325 330 335	1008
cgc ctg ctg gaa gat ggc gat ctc gag cca tct gct gga gac atg aga Arg Leu Leu Glu Asp Gly Asp Leu Glu Pro Ser Ala Gly Asp Met Arg 340 345 350	1056
gct gcc aac ctt tgg cca agc ccg ctc atg atc aaa cgc tct aag aag Ala Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys 355 360 365	1104
aac agc ctg gcc ttg tcc ctg acg gcc gac cag atg gtc agt gcc ttg Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu 370 375 380	1152
ttg gat gct gag ccc ccc ata ctc tat tcc gag tat gat cct acc aga Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg 385 390 395 400	1200
ccc ttc agt gaa gct tcg atg atg ggc tta ctg acc aac ctg gca gac Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp 405 410 415	1248

0085303-080601

gtg	gag	ctg	ggt	ctc	atg	atc	aac	tgg	gcg	aag	agg	gtg	cca	ggc	ttt	1296
Arg	Glu	Leu	Val	His	Met	Ile	Asn	Trp	Ala	Lys	Arg	Val	Pro	Gly	Phe	
			420					425					430			
gtg	gat	ttg	acc	ctc	cat	gat	cag	gtc	cac	ctt	cta	gaa	tgt	gcc	tgg	1344
Val	Asp	Leu	Thr	Leu	His	Asp	Gln	Val	His	Leu	Leu	Glu	Cys	Ala	Trp	
			435				440					445				
cta	gag	atc	ctg	atg	att	ggt	ctc	gtc	tgg	cgc	tcc	atg	gag	cac	cca	1392
Leu	Glu	Ile	Leu	Met	Ile	Gly	Leu	Val	Trp	Arg	Ser	Met	Glu	His	Pro	
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gtg	aag	cta	ctg	ttt	gct	cct	aac	ttg	ctc	ttg	gac	agg	aac	cag	gga	1440
Val	Lys	Leu	Leu	Phe	Ala	Pro	Asn	Leu	Leu	Leu	Asp	Arg	Asn	Gln	Gly	
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aaa	tgt	gta	gag	ggc	atg	gtg	gag	atc	ttc	gac	atg	ctg	ctg	gct	aca	1488
Lys	Cys	Val	Glu	Gly	Met	Val	Glu	Ile	Phe	Asp	Met	Leu	Leu	Ala	Thr	
				485					490					495		
tca	tct	cgg	ttc	cgc	atg	atg	aat	ctg	cag	gga	gag	gag	ttt	gtg	tgc	1536
Ser	Ser	Arg	Phe	Arg	Met	Met	Asn	Leu	Gln	Gly	Glu	Glu	Phe	Val	Cys	
			500				505						510			
ctc	aaa	tct	att	att	ttg	ctt	aat	tct	gga	gtg	tac	aca	ttt	ctg	tcc	1584
Leu	Lys	Ser	Ile	Ile	Leu	Leu	Asn	Ser	Gly	Val	Tyr	Thr	Phe	Leu	Ser	
			515				520				525					
agc	acc	ctg	aag	tct	ctg	gaa	gag	aag	gac	cat	atc	cac	cga	gtc	ctg	1632
Ser	Thr	Leu	Lys	Ser	Leu	Glu	Glu	Lys	Asp	His	Ile	His	Arg	Val	Leu	
			530			535					540					
gac	aag	atc	aca	gac	act	ttg	atc	cac	ctg	atg	gcc	aag	gca	ggc	ctg	1680
Asp	Lys	Ile	Thr	Asp	Thr	Leu	Ile	His	Leu	Met	Ala	Lys	Ala	Gly	Leu	
			545		550					555					560	
acc	ctg	cag	cag	cag	cac	cag	cgg	ctg	gcc	cag	ctc	ctc	ctc	atc	ctc	1728
Thr	Leu	Gln	Gln	Gln	His	Gln	Arg	Leu	Ala	Gln	Leu	Leu	Leu	Ile	Leu	
				565					570					575		
tcc	cac	atc	agg	cac	atg	agt	aac	aaa	ggc	atg	gag	cat	ctg	tac	agc	1776
Ser	His	Ile	Arg	His	Met	Ser	Asn	Lys	Gly	Met	Glu	His	Leu	Tyr	Ser	
			580				585						590			
atg	aag	tgc	aag	aac	gtg	gtg	ccc	ctc	tat	gac	ctg	ctg	ctg	gag	gcg	1824
Met	Lys	Cys	Val	Asn	Val	Val	Pro	Pro	Tyr	Asp	Leu	Leu	Leu	Glu	Ala	
			595			600					605					
gcg	gac	gcc	cac	cgc	cta	cat	gcg	ccc	act	agc	cgt	gga	ggg	gca	tcc	1872
Ala	Asp	Ala	His	Arg	Leu	His	Ala	Pro	Thr	Ser	Arg	Gly	Gly	Ala	Ser	
			610			615					620					
gtg	gag	gag	acg	gac	caa	agc	cac	ttg	gcc	act	gcg	ggc	tct	act	tca	1920
Val	Glu	Glu	Thr	Asp	Gln	Ser	His	Leu	Ala	Thr	Ala	Gly	Ser	Thr	Ser	
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Pro Ala Thr Ala
660

<220>
<223> Description of Artificial Sequence: Chimeric sequence
Homosapiens-Bacteriophage P1

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Asp	Ala	Thr	Ser	Asp	Glu	Val	Arg	Lys	Asn	Leu	Met	Asp	Met	Phe	Arg	
		20						25						30		
Asp	Arg	Gln	Ala	Phe	Ser	Glu	His	Thr	Trp	Lys	Met	Leu	Leu	Ser	Val	
		35					40					45				
Cys	Arg	Ser	Trp	Ala	Ala	Trp	Cys	Lys	Leu	Asn	Asn	Arg	Lys	Trp	Phe	
		50				55					60					
Pro	Ala	Glu	Pro	Glu	Asp	Val	Arg	Asp	Tyr	Leu	Leu	Tyr	Leu	Gln	Ala	
					70					75					80	
Arg	Gly	Leu	Ala	Val	Lys	Thr	Ile	Gln	Gln	His	Leu	Gly	Gln	Leu	Asn	
				85					90					95		
Met	Leu	His	Arg	Arg	Ser	Gly	Leu	Pro	Arg	Pro	Ser	Asp	Ser	Asn	Ala	
		100						105					110			
Val	Ser	Leu	Val	Met	Arg	Arg	Ile	Arg	Lys	Glu	Asn	Val	Asp	Ala	Gly	
		115					120					125				
Glu	Arg	Ala	Lys	Gln	Ala	Leu	Ala	Phe	Glu	Arg	Thr	Asp	Phe	Asp	Gln	
		130				135					140					
Val	Arg	Ser	Leu	Met	Glu	Asn	Ser	Asp	Arg	Cys	Gln	Asp	Ile	Arg	Asn	
					150					155					160	
Leu	Ala	Phe	Leu	Gly	Ile	Ala	Tyr	Asn	Thr	Leu	Leu	Arg	Ile	Ala	Glu	
				165					170					175		
Ile	Ala	Arg	Ile	Arg	Val	Lys	Asp	Ile	Ser	Arg	Thr	Asp	Gly	Gly	Arg	
			180					185					190			
Met	Leu	Ile	His	Ile	Gly	Arg	Thr	Lys	Thr	Leu	Val	Ser	Thr	Ala	Gly	
		195				200						205				

Val 210	Glu	Lys	Ala	Leu	Ser	Leu 215	Gly	Val	Thr	Lys	Leu 220	Val	Glu	Arg	Trp
Ile 225	Ser	Val	Ser	Gly	Val 230	Ala	Asp	Asp	Pro	Asn 235	Asn	Tyr	Leu	Phe	Cys 240
Arg	Val	Arg	Lys	Asn 245	Gly	Val	Ala	Ala	Pro 250	Ser	Ala	Thr	Ser	Gln 255	Leu
Ser	Thr	Arg	Ala 260	Leu	Glu	Gly	Ile	Phe 265	Glu	Ala	Thr	His	Arg 270	Leu	Ile
Tyr	Gly	Ala 275	Lys	Asp	Asp	Ser	Gly 280	Gln	Arg	Tyr	Leu	Ala 285	Trp	Ser	Gly
His 290	Ser	Ala	Arg	Val	Gly 295	Ala	Ala	Arg	Asp	Met	Ala 300	Arg	Ala	Gly	Val
Ser 305	Ile	Pro	Glu	Ile	Met 310	Gln	Ala	Gly	Gly	Trp 315	Thr	Asn	Val	Asn 320	Ile
Val	Met	Asn	Tyr	Ile 325	Arg	Asn	Leu	Asp	Ser 330	Glu	Thr	Gly	Ala	Met 335	Val
Arg	Leu	Leu 340	Glu	Asp	Gly	Asp	Leu	Glu 345	Pro	Ser	Ala	Gly	Asp 350	Met	Arg
Ala	Ala	Asn 355	Leu	Trp	Pro	Ser	Pro 360	Leu	Met	Ile	Lys	Arg 365	Ser	Lys	Lys
Asn 370	Ser	Leu	Ala	Leu	Ser 375	Leu	Thr	Ala	Asp	Gln	Met 380	Val	Ser	Ala	Leu
Leu 385	Asp	Ala	Glu	Pro	Pro 390	Ile	Leu	Tyr	Ser	Glu 395	Tyr	Asp	Pro	Thr	Arg
Pro	Phe	Ser	Glu	Ala 405	Ser	Met	Met	Gly	Leu 410	Leu	Thr	Asn	Leu	Ala	Asp
Arg	Glu	Leu 420	Val	His	Met	Ile	Asn	Trp 425	Ala	Lys	Arg	Val	Pro 430	Gly	Phe
Val	Asp	Leu 435	Thr	Leu	His	Asp	Gln 440	Val	His	Leu	Leu	Glu 445	Cys	Ala	Trp
Leu 450	Glu	Ile	Leu	Met	Ile	Gly 455	Leu	Val	Trp	Arg 460	Ser	Met	Glu	His	Pro
Val 465	Lys	Leu	Leu	Phe	Ala 470	Pro	Asn	Leu	Leu	Leu 475	Asp	Arg	Asn	Gln	Gly
Lys	Cys	Val	Glu	Gly 485	Met	Val	Glu	Ile	Phe 490	Asp	Met	Leu	Leu	Ala 495	Thr
Ser	Ser	Arg	Phe	Arg	Met	Met	Asn	Leu 505	Gln	Gly	Glu	Glu	Phe	Val	Cys

gat cgc cag gcg ttt tct gag cat acc tgg aaa atg ctt ctg tcc gtt 144
Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
35 40 45

tgc cgg tgc tgg gcg gca tgg tgc aag ttg aat aac cgg aaa tgg ttt 192
 Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
 50 55 60

ccc gca gaa cct gaa gat gtt cgc gat tat ctt cta tat ctt cag gcg 240
 Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala
 65 70 75 80

cgc ggt ctg gca gta aaa act atc cag caa cat ttg ggc cag cta aac 288
 Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn
 85 90 95

atg ctt cat cgt cgg tcc ggg ctg cca cga cca agt gac agc aat gct 336
 Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala
 100 105 110

gtt tca ctg gtt atg cgg cgg atc cga aaa gaa aac gtt gat gcc ggt 384
 Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly
 115 120 125

gaa cgt gca aaa cag gct cta gcg ttc gaa cgc act gat ttc gac cag 432
 Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln
 130 135 140

gtt cgt tca ctc atg gaa aat agc gat cgc tgc cag gat ata cgt aat 480
 Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
 145 150 155 160

ctg gca ttt ctg ggg att gct tat aac acc ctg tta cgt ata gcc gaa 528
 Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu
 165 170 175

att gcc agg atc agg gtt aaa gat atc tca cgt act gac ggt ggg aga 576
 Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg
 180 185 190

atg tta atc cat att ggc aga acg aaa acg ctg gtt agc acc gca ggt 624
 Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
 195 200 205

gta gag aag gca ctt agc ctg ggg gta act aaa ctg gtc gag cga tgg 672
 Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp
 210 215 220

att tcc gtc tct ggt gta gct gat gat cgg aat aac tac ctg ttt tgc 720
 Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys
 225 230 235 240

cgg gtc aga aaa aat ggt gtt gcc gcg cca tct gcc acc agc cag cta 768
 Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu
 245 250 255

tca act cgc gcc ctg gaa ggg att ttt gaa gca act cat cga ttg att 816
 Ser Thr Arg Ala Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Ile
 260 265 270

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Tyr	ggc	gct	aag	gat	gac	tct	ggt	cag	aga	tac	ctg	gcc	tgg	tct	gga	864
Gly	Ala	Lys	Asp	Asp	Ser	Gly	Gln	Arg	Tyr	Leu	Ala	Trp	Ser	Gly		
	275					280					285					
cac	agt	gcc	cgt	gtc	gga	gcc	gcg	cga	gat	atg	gcc	cgc	gct	gga	gtt	912
His	Ser	Ala	Arg	Val	Gly	Ala	Ala	Arg	Asp	Met	Ala	Arg	Ala	Gly	Val	
	290					295					300					
tca	ata	ccg	gag	atc	atg	caa	gct	ggt	ggc	tgg	acc	aat	gta	aat	att	960
Ser	Ile	Pro	Glu	Ile	Met	Gln	Ala	Gly	Gly	Trp	Thr	Asn	Val	Asn	Ile	
	305					310					315				320	
gtc	atg	aac	tat	atc	cgt	aac	ctg	gat	agt	gaa	aca	ggg	gca	atg	gtg	1008
Val	Met	Asn	Tyr	Ile	Arg	Asn	Leu	Asp	Ser	Glu	Thr	Gly	Ala	Met	Val	
				325					330					335		
cgc	ctg	ctg	gaa	gat	ggc	gat	ctc	gag	cca	tct	gct	gga	gac	atg	aga	1056
Arg	Leu	Leu	Glu	Asp	Gly	Asp	Leu	Glu	Pro	Ser	Ala	Gly	Asp	Met	Arg	
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gct	gcc	aac	ctt	tgg	cca	agc	ccg	ctc	atg	atc	aaa	cgc	tct	aag	aag	1104
Ala	Ala	Asn	Leu	Trp	Pro	Ser	Pro	Leu	Met	Ile	Lys	Arg	Ser	Lys	Lys	
		355					360					365				
aac	agc	ctg	gcc	tgt	tcc	ctg	acg	gcc	gac	cag	atg	gtc	agt	gcc	tgt	1152
Asn	Ser	Leu	Ala	Leu	Ser	Leu	Thr	Ala	Asp	Gln	Met	Val	Glc	Ser	Ala	
	370						375				380					
ttg	gat	gct	gag	ccc	ccc	ata	ctc	tat	tcc	gat	tat	gat	cct	acc	aga	1200
Leu	Asp	Ala	Glu	Pro	Pro	Ile	Leu	Tyr	Ser	Glu	Tyr	Asp	Pro	Thr	Arg	
	385					390					395				400	
ccc	ttc	agt	gaa	gct	tcg	atg	atg	ggc	tta	ctg	acc	aac	ctg	gca	gac	1248
Pro	Phe	Ser	Glu	Ala	Ser	Met	Met	Gly	Leu	Leu	Thr	Asn	Leu	Ala	Asp	
			405						410					415		
agg	gag	ctg	gtt	cac	atg	atc	aac	tgg	gcg	aag	agg	gtg	cca	ggc	ttt	1296
Arg	Glu	Leu	Val	His	Met	Ile	Asn	Trp	Ala	Lys	Arg	Val	Pro	Gly	Phe	
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gtg	gat	ttg	acc	ctc	cat	gat	cag	gtc	cac	ctt	cta	gaa	gtg	gcc	tgg	1344
Val	Asp	Leu	Thr	Leu	His	Asp	Gln	Val	His	Leu	Leu	Glu	Cys	Ala	Trp	
			435					440					445			
cta	gag	atc	ctg	atg	att	ggc	ctc	gtc	tgg	cgc	tcc	atg	gag	cac	cca	1392
Leu	Glu	Ile	Leu	Met	Ile	Gly	Leu	Val	Trp	Arg	Ser	Met	Glu	His	Pro	
			450			455						460				
ggg	aag	cta	ctg	ttt	gct	cct	aac	ttg	ctc	ttg	gac	agg	aac	cag	gga	1440
Gly	Lys	Leu	Leu	Phe	Ala	Pro	Asn	Leu	Leu	Leu	Asp	Arg	Asn	Gln	Gly	
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aaa	tgt	gta	gag	ggc	atg	gtg	gag	atc	ttc							

Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val
1 5 10 15

Asp	Ala	Thr	Ser	Asp	Glu	Val	Arg	Lys	Asn	Leu	Met	Asp	Met	Phe	Arg
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Asp	Arg	Gln	Ala	Phe	Ser	Glu	His	Thr	Trp	Lys	Met	Leu	Leu	Ser	Val
		35					40					45			
Cys	Arg	Ser	Trp	Ala	Ala	Trp	Cys	Lys	Leu	Asn	Asn	Arg	Lys	Trp	Phe
	50					55				60					
Pro	Ala	Glu	Pro	Glu	Asp	Val	Arg	Asp	Tyr	Leu	Leu	Tyr	Leu	Gln	Ala
	65				70					75				80	
Arg	Gly	Leu	Ala	Val	Lys	Thr	Ile	Gln	Gln	His	Leu	Gly	Gln	Leu	Asn
				85				90						95	
Met	Leu	His	Arg	Arg	Ser	Gly	Leu	Pro	Arg	Pro	Ser	Asp	Ser	Asn	Ala
			100					105					110		
Val	Ser	Leu	Val	Met	Arg	Arg	Ile	Arg	Lys	Glu	Asn	Val	Asp	Ala	Gly
		115					120					125			
Glu	Arg	Ala	Lys	Gln	Ala	Leu	Ala	Phe	Glu	Arg	Thr	Asp	Phe	Asp	Gln
	130					135					140				
Val	Arg	Ser	Leu	Met	Glu	Asn	Ser	Asp	Arg	Cys	Gln	Asp	Ile	Arg	Asn
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Leu	Ala	Phe	Leu	Gly	Ile	Ala	Tyr	Asn	Thr	Leu	Leu	Arg	Ile	Ala	Glu
			165						170					175	
Ile	Ala	Arg	Ile	Arg	Val	Lys	Asp	Ile	Ser	Arg	Thr	Asp	Gly	Gly	Arg
		180						185					190		
Met	Leu	Ile	His	Ile	Gly	Arg	Thr	Lys	Thr	Leu	Val	Ser	Thr	Ala	Gly
		195				200						205			
Val	Glu	Lys	Ala	Leu	Ser	Leu	Gly	Val	Thr	Lys	Leu	Val	Glu	Arg	Trp
	210					215					220				
Ile	Ser	Val	Ser	Gly	Val	Ala	Asp	Asp	Pro	Asn	Asn	Tyr	Leu	Phe	Cys
	225			230						235				240	
Arg	Val	Arg	Lys	Asn	Gly	Val	Ala	Ala	Pro	Ser	Ala	Thr	Ser	Gln	Leu
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Ser	Thr	Arg	Ala	Leu	Glu	Gly	Ile	Phe	Glu	Ala	Thr	His	Arg	Leu	Ile
			260					265					270		
Tyr	Gly	Ala	Lys	Asp	Asp	Ser	Gly	Gln	Arg	Tyr	Leu	Ala	Trp	Ser	Gly
	275					280						285			
His	Ser	Ala	Arg	Val	Gly	Ala	Ala	Arg	Asp	Met	Ala	Arg	Ala	Gly	Val
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Ser	Ile	Pro	Glu	Ile	Met	Gln	Ala	Gly	Gly	Trp	Thr	Asn	Val	Asn	Ile
	305				310					315				320	

Val	Met	Asn	Tyr	Ile	Arg	Asn	Leu	Asp	Ser	Glu	Thr	Gly	Ala	Met	Val
				325					330					335	
Arg	Leu	Leu	Glu	Asp	Gly	Asp	Leu	Glu	Pro	Ser	Ala	Gly	Asp	Met	Arg
			340					345					350		
Ala	Ala	Asn	Leu	Trp	Pro	Ser	Pro	Leu	Met	Ile	Lys	Arg	Ser	Lys	Lys
		355					360					365			
Asn	Ser	Leu	Ala	Leu	Ser	Leu	Thr	Ala	Asp	Gln	Met	Val	Ser	Ala	Leu
		370				375					380				
Leu	Asp	Ala	Glu	Pro	Pro	Ile	Leu	Tyr	Ser	Glu	Tyr	Asp	Pro	Thr	Arg
385					390					395					400
Pro	Phe	Ser	Glu	Ala	Ser	Met	Met	Gly	Leu	Leu	Thr	Asn	Leu	Ala	Asp
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Arg	Glu	Leu	Val	His	Met	Ile	Asn	Trp	Ala	Lys	Arg	Val	Pro	Gly	Phe
			420					425					430		
Val	Asp	Leu	Thr	Leu	His	Asp	Gln	Val	His	Leu	Leu	Glu	Cys	Ala	Trp
			435				440					445			
Leu	Glu	Ile	Leu	Met	Ile	Gly	Leu	Val	Trp	Arg	Ser	Met	Glu	His	Pro
						455					460				
Gly	Lys	Leu	Leu	Phe	Ala	Pro	Asn	Leu	Leu	Leu	Asp	Arg	Asn	Gln	Gly
465					470					475				480	
Lys	Cys	Val	Glu	Gly	Met	Val	Glu	Ile	Phe	Asp	Met	Leu	Leu	Ala	Thr
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Ser	Ser	Arg	Phe	Arg	Met	Met	Asn	Leu	Gln	Gly	Glu	Glu	Phe	Val	Cys
			500					505					510		
Leu	Lys	Ser	Ile	Ile	Leu	Leu	Asn	Ser	Gly	Val	Tyr	Thr	Phe	Leu	Ser
		515					520					525			
Ser	Thr	Leu	Lys	Ser	Leu	Glu	Glu	Lys	Asp	His	Ile	His	Arg	Val	Leu
		530				535					540				
Asp	Lys	Ile	Thr	Asp	Thr	Leu	Ile	His	Leu	Met	Ala	Lys	Ala	Gly	Leu
545					550					555					560
Thr	Leu	Gln	Gln	Gln	His	Gln	Arg	Leu	Ala	Gln	Leu	Leu	Leu	Ile	Leu
				565					570					575	
Ser	His	Ile	Arg	His	Met	Ser	Asn	Lys	Gly	Met	Glu	His	Leu	Tyr	Ser
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Met	Lys	Cys	Lys	Asn	Val	Val	Pro	Leu	Tyr	Asp	Leu	Leu	Leu	Glu	Ala
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Ala	Asp	Ala	His	Arg	Leu	His	Ala	Pro	Thr	Ser	Arg	Gly	Gly	Ala	Ser
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<213> Mus musculus

<400> 14

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37

102080.20000000